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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gardner S.M., Mock B.A., Hilgers J., Huppi K.E., Roeder W.D.; Mouse lymphotoxin and tumor necrosis factor: structural analysis of the cloned genes, physical linkage, and chromosomal position."; J. Immunol. 139:476-481(1987).
                                                                                                                                                                                                                                                                                                        Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R., Batchofffe A., Loretz C., Lasky S., Hood L., "Sequence of the mouse major histocompatibility class III region."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SECURNCE OF 6-202 FROM N.A. MEDLINE=89144552; PLDMEd=3147435; PEDLINE=89144562; PLDMEd=3147435; PEDLINE=80144562; PLDMEd=3147435; PEDLINE=80147F.; PEDLINE=8014F.; PEDLINE=8014F.; PEDLINE=8014F.; PEDLINE=8014F. PEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
associated (heterotrimers) (By similarity).
-}- SIMILARITY: Belongs to the tumor necrosis factor family.
"Cloning and expression of murine lymphotoxin cDNR."; J. Immunol. 138:4496-4501(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO, GO:0006959; P:humoral immune response; IMP. GO; GO:000515; P:lymmp qland development; IMP. InterPro; IPR006053; TNF abc.
InterPro; IPR006053; TNF Eamily.
InterPro; IPR008981; TNF Like.
InterPro; IPR008981; TNF Like.
InterPro; IPR003681; TNF Like.
Ffam; PF00229; TNF: 1.
PF1090; PF002012; TNF; TNECROSISFCT.
Probom; PF002012; TNF; Subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                 MEDLINE=87252204; PubMed=2885372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U06950; AAA18593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene Res. 3:409-414(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; AAA39450.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA68330.1; -.
AAA40460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAA29567.1;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF
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	2,	190	244	
•	Gaps	133 HPEPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVILSGVKYKKGGLVINETGLYF 190 46 HPLPQKHLTHGILKPAAHLVGYPSKQNSLLMRASTDRAFLRHGFSLSNNSLLIPTSGLYF 105	VYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGROMSYCTTGOMMARSSY 244	
ને	8,	TINE	CPW7	
NTIA		GGLV - NSLI	CTTG	
atoq .	ngth 20 Indels	KYKK	XSAX	
F 1; 1. F 2; 1. 33 LYMPHOTOXIN-ALPHA. 02 N-LINXED GLCHAC) (POTENTIAL) 25 A -> P (IN REP. 5). 62 VR -> CG (IN REP. 5). 21998 MW; F496F83C68S950D3 CRC64;	13.4%; Score 204; DB 1; Length 202; 32.5%; Pred. No. 1.5e-07; ive 25; Mismatches 73; Indels	LSGV - RHGF		<u> </u>
# :: 6 :: 0 . 5 : 0 . 5 : 0 . 5 : 0	73; 73;	GIVI	DLVP.	4-4 % %
ALPH CINAC EF. FREF	DB 1 Se-0	EDTY - PASTD	KYPC 	GLY3
1. LYMPHOTOXIN-ALPHA. N-LINXED (GLCKAC. N-P (IN REF. 5). VR -> CG (IN REF. 2). R496F83C685950D3 (24 / 2. 1. ttche	PLEAT	MRNS : : DLFSS	SOFF
PHOTC INKEI PP CC 196F6	re 2(NSRSI SKON	SHKV 	NFEE
LLYMI LLYMI N-EJ N-EJ VR -	Score 204; DB 1; Le Pred. No. 1.5e-07; 25; Mismatches 73;	IGKS)	NLPL!	LSLV : : ISHL
1. 1. Signa	4.4. 4.7.	HE H	AIPT	NVSE: HTDG
PSC0251; TNF 1; 1 PSSC049; TNF 2; 1 Glycoprocein; Si; 3 34 202 93 93 93 56 26 161 162 202 AA; 21998	larity 32.3 Conservative	-LRY	CS PR	245 LGAVFNLTSADHLYVNVSELSLYNFEESQTFFGLYKL 281 : : : : : : :
rote.	ty erva	KKE-	RGOSCN : : SGESCS	TSAD : SKGD
00251; 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	lari Cons	PPPE POKH	SKVYF : rsovvF	VENT TIME
PSS	h Simi 51,	HPS HPL		3=8
PROSITE; PS00251; TNF 1; 1. PROSITE; PS50049; TNF 2; 1. Cytckine; Glycoprotein; Signal. 31 202 CHAIN 34 202 CHAIN 93 93 N- CONFLICT 26 26 A CONFLICT 161 162 COMPLICT 161 162 SEQUENCE 202 AA; 21998 MM;	atch cal	133	191	245
PROSI PROSI CYTOK SIGNA CHAIN CARBO CONFL CONFL	Query Match Best Local Similarity Matches 51; Conserv			
DR DR FT FT SO	Que Bes Mat	දු පු	දු දු	දු දු

Page macrophage; memb macrophage 70 A;Introns: 33/3; 69/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophag
F;1-34,Domain: signal sequence #status predicted <SIG>
F;35-205/Product: lymphotoxin #status predicted <AMITF;41/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;96/Binding site: carbohydrate (Abn) (covalent) 125 SSLRKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEW-EDTYGIVLLSGVKYKKGGLVI 183 PLDGLYLIYSQVLFKGQGCPSTHVLLTHTISRLAVSYPSKVNLLSA-IKSPCHTESPEQA 186 140 KKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRG 199 60 --TLKPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSG 117 Q----SCHNLPLSHKYYMRNSKYPQDLVMMEGRMMSYCTTGQMWARSSYLGAVFNLTS 253 75 tumor Alternate names: cachectin; TMF alpha Species: Equus caballus (domestic horse) Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000 20 KAGGPQGSRRCLCLSIFSFL--LVAGATTLFCLLHFGVIGPQREBQLPNAFQSINPL--A 76 OTLRSSSRTPBDKP-----VAHVVANPQAEGO-LOWLSGRANALLANGVKLTDNQLVV 184 NETGLYFVYSKVYFRGQSC--NNLPLSHKYTWRNSKYPQDLVMMEGKMMSYCTT-------OKELAELRESTSOMHTA 57; Conservative 33; Mismatches 90; Indels 28; Gaps 91; CLLYWFFWVLVALVGL-GLGMFQLFHLGKELARLRESTSQMHTASSLEKGIGHPSPPPB Gaps Accession: JQ1344.
Molecule type: DNA.
Molecule type: DNA.
Residues: 1-234 <GUNA.
COSS-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245.
COMMENT: This protein is an important proximal mediator of endotoxemia. Aintrons: 62/3; 79/1; 95/1 G)Superfantly: tumor necrosis factor G)Superfantly: tumor necrosis factor G)Keywords: cytcokine; cytcokine; glycoprotein; lipoprotein; lymphokine; F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM> F;19,20/Binding site: myristate (fyrs) (covalent) #status predicted F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted F;146-178/Disulfide bonds: #status predicted equine Length 234; encoding DB 1; Length 205; -GOMMARSSYLCAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL : Indels Indels TITE: Cloning and characterization of gene TNF alpha Reference number: JQ1344; MUID:92084125; PMID:1748301 Query Match
12.2%; Score 186.5; DB 1;
Best Local Similarity 27.2%; Pred. No. 1.1e-06;
Matches 62; Conservative 36; Mismatches 99; 72 KKRGNHSTGLCLLVMPFMVLVALVGLGLGMFQLFHL---Query Match
12.5%; Score 191; DB 1;
Best Local Similarity 27.4%; Pred. No. 4.4e-07;
Matches 57; Conservative 33; Mismatches 90 205 horse GDOLSTHIDGIPHLVLSPSTVFFGAPAL necrosis factor alpha precursor , Morris, D.D.; McGraw, R.A. A, Gene: TNF-alpha 200 Genetics: a ò 셤 ò ሯ 셤 ઠે d ઠે d ò В à 셤 δ). Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction, while having no detrimental effect on normal cells. It can also act synergistically wit b.Comment: This protein and TNP-alpha (tumor necrosis factor) are the products of differ can activities but are produced by different cell types and have different induction kignbetis: Lesidues: 1-59, NV, 61-205 <KOB>
Loss-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914

Loss-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914

Lote: the authors translated the codon TAT for residue 156 as Thr and ACC for residue 100 authors 5.; Ando, 5.; Sanou, 0.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; AT phobine Res. 7, 175-185, 1988

Litle: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and eference number: A61478; MUID:88301617; PMID:2841543 Molecule type: protein Residues: 56-79186-95, X', 97, X', 99;119-151, XX', 154-162, X', 164, X', 166, X', 168, X', 1 Residues: 56-79186-95 Woigt, C.G.; Maurer-Poyy, I.; Adolf, G.R. BBS Lett. 314, 85-88, 1992 Thitle: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylatid Reference number: \$26951; MUID:93083656; PMID:1451807 Accession: \$26951 뜅 Ä OSSE-references: CB:X01393; NID:93444; PIDN:CAA25649.1; PID:934445

perimental source: lymphoblastoid cell line RPMI-1788

seddel, D.V.; Aggarval, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.A.

Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986

Itle: Tumor necrosis factors: gene structure and biological activities.

sference number: A32877; MUID:87217059; PMID:3472740

ccession: B32877

ccession: preliminary; not compared with conceptual translation le: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour erence number: A93350; MUID:85086243; PMID:6334807 Jarrett, J.A. cell ukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K. h. Biochem. Biophys. 304, 144-153, 1993
itle: N-linked sugar. Chain structure of recombinant human lymphotoxin produced by eference number: \$34742; WUID:93311995; PMID:8323280 "Molecule type: DNA 14-205 <IRI>
"Readduces 1-12, R", 14-205 <IRI>"Facaiduces 1-12, R", 14-205 (IRI)
"Readduces 1-12, R", 14-205 (IRI)
"Readduces references EMBL: 215026; NID: g37211; PIDN: CAA78746.1; PID: g37213
Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
N, Mote: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
"Machana, LJ'; Du, D.C., Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
"Immunogenetics 33, 50-53, 1991
N, Title: Haplotypic polymorphisms of the TNFB gene.
N, Title: Haplotypic polymorphisms of the TNFB gene. ozyashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T. ochem. 100, 727-733, 1986 1le: Cloning and expression of human lymphotoxin mRNA derived from a human exence number: A91906; MUID:87057135; PMID:3536896 Residues: 1-124, P',126-205 <RES>
(Cross-references: GB:MS5913; NID:G339742; PIDN:AAB59455.1; PID:G339743; Experimental source: ancestral haplotype 57.1
Note: 59-Asm was also found (ancestral hablotype 8.1) translation not shown translation not shown; translated from GB/EMBL/DDBJ . F.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S. C:Genetics: A/Gene: GDB:LTA, LT, TNFB A/CTOSS=Keterences: GDB:120442; OMIM:153440 A/Map posicion: 6p21.3-6p21.3 nucleic acid sequence not shown;

ecule type: mRNA idues: 35-205 <GOE>

ecule type: mRNA

:88ion: A91906

Accession: A61478

cule type: mRNA dues: 1-205 <GRA>

Accession: A93350

ecule type: DNA

Accession: 154482

Molecule type: protein Residues: 35-59,'N',61-205 <VOI>>Note: 60-Thr was also found

Reference number: S34 Contents: annotation

Dense Alu clustering and a potential new member of the NPKappaB family within nnce number: S36152; MUID:93272029; PMID:8499947

234

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Page 3 61 PPLPPLPLPPLXCRGNHSTGLCLLVMFFWTLVALVGLGLGMPQLFHLQKELABLRESTSQ 120 61 PPLPPLENCKGNHSTGLCLUWFFWULVALVGLGLGMPQLFHLQXELAEJRRSTSQ 120 121 MHTASSL----GHPSPPPEKKELRKVAHLIGKSNSRSMPLEWEDIYGIVLLSGVKYKKGG 176 177 LVINETGLYFVYSKVYFRGQSCHALPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWA 236 181 LVINETGEYFVYSKVYFRGQSCNNLFLSHKVYMRNSKYPQDLVMMEGKAMSYCTTGQMMA 240 237 RSSYLGAVENLISADHLYVNVSELSLVNFBESQTFFGLYKL 277 a-2.rapb 8 6 6 6 6 දි දි 8 121 MHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGG 180 181 LVINETGLYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMMA 240 121 MHTASSI----GHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGG 176 1 MODENYPPOLYWIDSBASSPARPOTYL-CFSSIPRREGGREPSPEPPLEPEPP 60
1 MODENYPPOLYWIDSBASSPARSPARPOTYL-CFSSIPRREGGREPSPEPPPEPPEP 60 hang, Jun. Thirth, Stephen Amin, Wifen Apoptoesis Inducing Molecule II and Methods of Use 27.21 1489.0650006 CCATION NUMBER: US/09/252,656B Owery Match 99.2*, Score 1492; DB 9; Length 281; Best Local Similarity 98.6*; Pred. No. 2.3e-104. Matches 277; Conservative 0; Mismatches 0; Indals Matches 277; Conservative 0; Mismatches 0; Indals Length 281; Ouery Match 99.2%; Score 1492; DB 9; Best Local Similarity 98.6%; Pred. No. 2.3e-105; Matches 277; CgpServative 0; Mismatches 0; 45 DATE: 1999-02-19 VITON NUMBER: US 60/075,409 DATE: 1998-02-20 09/027,287 09/003,886 08/822,953 NUMBER OF SEQ ID NOS: 61 | SOFTHARE: Patentin versit | SEQ ID NO | | LENGTH: 21 | TYPE: PFT HOME SADIES | ON-252-668-6

.88.0650004 DN NUMBER: US/09/027,287A

Query Match
Best Local Similarity 91.8%; Pred. No. 3.6
Matches 258; Conservative 0; Mismatches